

**Table S1. Regions of allelic imbalance imposed to the HapMap sample NA06991<sup>a</sup>**

Region	Aberration Type <sup>b</sup>	Chr <sup>c</sup>	bp Start <sup>c</sup>	bp End <sup>c</sup>	#SNP <sup>d</sup>	#hetSNP <sup>d</sup>
1	CN-LOH	5	1	47700000	9397	2756
2	Loss	5	111789971	112521346	156	79
3	Gain	8	1	45200000	12564	3830
4	Gain	8	128432670	129207869	218	91
5	Loss	9	1	50600000	11201	3889
6	Loss	10	84504379	94825178	1988	648
7	Gain	12	1	132449811	27131	8818
8	Loss	13	31766569	31892852	37	10
9	CN-LOH	17	7431864	11747138	1150	308
10	CN-LOH	17	22300000	78774742	9713	3205
Total number of modified heterozygous SNPs						23634
Total number of heterozygous SNPs on autosome						176207
Total number of SNPs on autosome						547359

a: For more details, see Staaf J, et al. (2008) Genome Biology 9: R136.

b: Aberration type includes one-copy gain/loss and copy-neutral loss of heterozygosity (CN-LOH).

c: Chromosome and base pair start/end position where each simulated region is located.

d: Listed is the number of SNPs and those with heterozygous genotypes within each region.